

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/489,850

DATE: 08/28/2001  
TIME: 09:09:33

Input Set : N:\Crf3\RULE60\09489850.txt  
Output Set: N:\CRF3\08282001\I489850.raw

## SEQUENCE LISTING

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1645

pdf#4

## 4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: VAN ALSTYNE, Diane  
7 SHARMA, Lawrence Rajendra  
9 (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
10 BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
11 CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
13 (iii) NUMBER OF SEQUENCES: 75  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: Foley & Lardner  
17 (B) STREET: 3000 K Street, N.W., Suite 500  
18 (C) CITY: Washington  
19 (D) STATE: D.C.  
20 (E) COUNTRY: USA  
21 (F) ZIP: 20007-5109  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
29 (vi) CURRENT APPLICATION DATA:  
C--> 30 (A) APPLICATION NUMBER: US/09/489,850  
C--> 31 (B) FILING DATE: 24-Jan-2000  
32 (C) CLASSIFICATION:  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: 08/988,444  
36 (B) FILING DATE:  
38 (A) APPLICATION NUMBER: US 08/127,499  
39 (B) FILING DATE: 28-SEP-1993  
41 (viii) ATTORNEY/AGENT INFORMATION:  
42 (A) NAME: BENT, Stephen A.  
43 (B) REGISTRATION NUMBER: 29,768  
44 (C) REFERENCE/DOCKET NUMBER: 51916/103/INBI  
46 (ix) TELECOMMUNICATION INFORMATION:  
47 (A) TELEPHONE: (202)672-5300  
48 (B) TELEFAX: (202)672-5399  
49 (C) TELEX: 904136

ENTERED

## 52 (2) INFORMATION FOR SEQ ID NO: 1:

- 54 (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 992 amino acids  
56 (B) TYPE: amino acid  
57 (C) STRANDEDNESS:  
58 (D) TOPOLOGY: unknown  
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
66 Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu  
67 1 5 10 15  
69 Glu Ala Gln Ser Arg Ala Leu Arg Ala Gly Leu Ala Ala Gly Ala Ser

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70		20		25		30										
72	Gln	Ser	Arg	Arg	Pro	Arg	Pro	Arg	His	Ala	Arg	Leu	Gln	His	I	
73		35		40		45										
75	Pro	Glu	Met	Thr	Pro	Ala	Val	Thr	Pro	Glu	Gly	Pro	Ala	Pro	Pro	Arg
76		50		55		60										
78	Thr	Gly	Ala	Trp	Gln	Arg	Lys	Asp	Trp	Ser	Arg	Ala	Pro	Pro	Pro	Pro
79	65			70		75		80								
81	Glu	Glu	Arg	Gln	Glu	Ser	Arg	Ser	Gln	Thr	Pro	Ala	Pro	Lys	Pro	Ser
82				85		90		95								
84	Arg	Ala	Pro	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Arg	Met	Gln	Thr	Gly	Arg
85				100		105		110								
87	Gly	Gly	Ser	Ala	Pro	Arg	Pro	Glu	Leu	Gly	Pro	Pro	Thr	Asn	Pro	Phe
88				115		120		125								
90	Gln	Ala	Ala	Val	Ala	Arg	Gly	Leu	Arg	Pro	Pro	Leu	His	Asp	Pro	Asp
91				130		135		140								
93	Thr	Glu	Ala	Pro	Thr	Glu	Ala	Cys	Val	Thr	Ser	Trp	Leu	Trp	Ser	Glu
94	145					150					155					160
96	Gly	Glu	Gly	Ala	Val	Phe	Tyr	Arg	Val	Asp	Leu	His	Phe	Ile	Asn	Leu
97				165		170		175								
99	Gly	Thr	Pro	Pro	Leu	Asp	Glu	Asp	Gly	Arg	Trp	Asp	Pro	Ala	Leu	Met
100				180		185		190								
102	Tyr	Asn	Pro	Cys	Gly	Pro	Glu	Pro	Pro	Ala	His	Val	Val	Arg	Ala	Ty
103				195		200		205								
105	Asn	Gln	Pro	Ala	Gly	Asp	Val	Arg	Gly	Val	Trp	Gly	Lys	Gly	Glu	Arg
106				210		215		220								
108	Thr	Tyr	Ala	Glu	Gln	Asp	Phe	Arg	Val	Gly	Gly	Thr	Arg	Trp	His	Arg
109	225					230					235					240
111	Leu	Leu	Arg	Met	Pro	Val	Arg	Gly	Leu	Asp	Gly	Asp	Thr	Ala	Pro	Leu
112				245		250		255								
114	Pro	Pro	His	Thr	Thr	Glu	Arg	Ile	Glu	Thr	Arg	Ser	Ala	Arg	His	Pro
115				260		265		270								
117	Trp	Arg	Ile	Arg	Phe	Gly	Ala	Pro	Gln	Ala	Phe	Leu	Ala	Gly	Leu	Leu
118				275		280		285								
120	Leu	Ala	Ala	Val	Ala	Val	Gly	Thr	Ala	Arg	Ala	Gly	Leu	Gln	Pro	Arg
121				290		295		300								
123	Ala	Asp	Met	Ala	Ala	Pro	Pro	Met	Pro	Pro	Gln	Pro	Pro	Arg	Ala	His
124	305					310					315					320
126	Gly	Gln	His	Tyr	Gly	His	His	His	His	Gln	Leu	Pro	Phe	Leu	Gly	His
127				325		330		335								
129	Asp	Gly	His	His	Gly	Gly	Thr	Leu	Arg	Val	Gly	Gln	His	His	Arg	Asn
130				340		345		350								
132	Ala	Ser	Asp	Val	Leu	Pro	Gly	His	Trp	Leu	Gln	Gly	Gly	Trp	Gly	Cys
133				355		360		365								
135	Tyr	Asn	Leu	Ser	Asp	Trp	His	Gln	Gly	Thr	His	Val	Cys	His	Thr	Lys
136				370		375		380								
138	His	Met	Asp	Phe	Trp	Cys	Val	Glu	His	Asp	Arg	Pro	Pro	Pro	Ala	Thr
139	385					390					395					400
141	Pro	Thr	Ser	Leu	Thr	Thr	Ala	Ala	Asn	Tyr	Ile	Ala	Ala	Ala	Thr	Pro
142				405		410		415								

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```

144   Ala Thr Ala Pro Pro Pro Cys His Ala Gly Leu Asn Asp Ser Cys Gly
145           420           425           430
147   Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Pro Thr Ala Leu Thr
148           435           440           445
150   Pro Gly Ala Val Gly Asp Leu Arg Ala Val His His Arg Pro Val Pro
151           450           455           460
153   Ala Tyr Pro Val Cys Cys Ala Met Arg Trp Gly Leu Pro Pro Trp Glu
154           465           470           475           480
156   Leu Val Ile Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys Arg Gly
157           485           490           495
159   Val Pro Ala His Pro Gly Thr Arg Cys Pro Glu Leu Val Ser Pro Met
160           500           505           510
162   Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala Thr Ala
163           515           520           525
165   Asn Ala Leu Ser Leu Asp His Ala Phe Ala Ala Phe Val Leu Leu Val
166           530           535           540
168   Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg Arg Pro
169           545           550           555           560
171   Ala Pro Pro Pro Pro Ser Pro Gln Ser Ser Cys Arg Gly Thr Thr Pro
172           565           570           575
174   Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala Pro Gly
175           580           585           590
177   Cys Ala Thr Gln Thr Pro Val Pro Val Arg Leu Ala Gly Val Gly Phe
178           595           600           605
180   Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp Leu Glu
181           610           615           620
183   Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser Cys Glu
184           625           630           635           640
186   Gly Leu Gly Ala Trp Val Pro Thr Ala Pro Cys Ala Arg Ile Trp Asn
187           645           650           655
189   Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr Ser Ser
190           660           665           670
192   Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly Ser Tyr
193           675           680           685
195   Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala Phe Gly
196           690           695           700
198   His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val Met Ser
199           705           710           715           720
201   Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr Val Arg
202           725           730           735
204   Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser Val Ala
205           740           745           750
207   Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn Thr Pro
208           755           760           765
210   His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp Leu Val
211           770           775           780
213   Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp Gly Leu
214           785           790           795           800
216   Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val Cys Gln

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```

217          805          810          815
219  Arg His Ser Pro Asp Cys Ser Arg Leu Val Gly Ala Thr Pro Glu Arg
220          820          825          830
222  Pro Arg Leu Arg Leu Val Asp Ala Asp Asp Pro Leu Leu Arg Thr Ala
223          835          840          845
225  Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val Ile Gly Ser Gln Ala
226          850          855          860
228  Arg Lys Cys Gly Leu His Ile Arg Ala Gly Pro Tyr Gly His Ala Thr
229          865          870          875          880
231  Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp Pro Trp
232          885          890          895
234  His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg Pro Val
235          900          905          910
237  Ala Leu Pro Arg Ala Leu Ala Pro Pro Arg Asn Val Arg Val Thr Gly
238          915          920          925
240  Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala Pro Gly
241          930          935          940
243  Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly Ala Phe
244          945          950          955          960
246  Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro Pro Pro
247          965          970          975
249  Tyr Gln Val Ser Cys Gly Gly Glu Ser Asp Arg Ala Ser Ala Gly His
250          980          985          990

```

## 253 (2) INFORMATION FOR SEQ ID NO: 2:

## 255 (i) SEQUENCE CHARACTERISTICS:

256 (A) LENGTH: 21 amino acids

257 (B) TYPE: amino acid

258 (C) STRANDEDNESS:

259 (D) TOPOLOGY: unknown

## 265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

267 Pro Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr

268 1 5 10 15

270 Gly Arg Gly Gly Ser

271 20

## 273 (2) INFORMATION FOR SEQ ID NO: 3:

## 275 (i) SEQUENCE CHARACTERISTICS:

276 (A) LENGTH: 7 amino acids

277 (B) TYPE: amino acid

278 (C) STRANDEDNESS:

279 (D) TOPOLOGY: unknown

## 285 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

287 Gln Pro Gln Pro Pro Arg Met

288 1 5

## 290 (2) INFORMATION FOR SEQ ID NO: 4:

## 292 (i) SEQUENCE CHARACTERISTICS:

293 (A) LENGTH: 21 amino acids

294 (B) TYPE: amino acid

295 (C) STRANDEDNESS:

296 (D) TOPOLOGY: unknown

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```

302 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
304 Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg
305 1 5 10 15
307 Ala Pro Pro Gln Gln
308 20
310 (2) INFORMATION FOR SEQ ID NO: 5:
312 (i) SEQUENCE CHARACTERISTICS:
313 (A) LENGTH: 7 amino acids
314 (B) TYPE: amino acid
315 (C) STRANDEDNESS:
316 (D) TOPOLOGY: unknown
322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
324 Gln Thr Pro Ala Pro Lys Pro
325 1 5
327 (2) INFORMATION FOR SEQ ID NO: 6:
329 (i) SEQUENCE CHARACTERISTICS:
330 (A) LENGTH: 21 amino acids
331 (B) TYPE: amino acid
332 (C) STRANDEDNESS:
333 (D) TOPOLOGY: unknown
339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
341 Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly
342 1 5 10 15
344 Gln His Tyr Gly His
345 20
347 (2) INFORMATION FOR SEQ ID NO: 7:
349 (i) SEQUENCE CHARACTERISTICS:
350 (A) LENGTH: 7 amino acids
351 (B) TYPE: amino acid
352 (C) STRANDEDNESS:
353 (D) TOPOLOGY: unknown
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
361 Pro Pro Gln Pro Pro Arg Ala
362 1 5
364 (2) INFORMATION FOR SEQ ID NO: 8:
366 (i) SEQUENCE CHARACTERISTICS:
367 (A) LENGTH: 1063 amino acids
368 (B) TYPE: amino acid
369 (C) STRANDEDNESS:
370 (D) TOPOLOGY: unknown
376 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
378 Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
379 1 5 10 15
381 Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser
382 20 25 30
384 Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser
385 35 40 45
387 Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Arg Gly
388 50 55 60

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/489,850

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Input Set : N:\Crf3\RULE60\09489850.txt

Output Set: N:\CRF3\08282001\I489850.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23

L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23